<400> 1
gacccacgcg tccggccggc ccttctcttc ccttgctgct gtgcgaaccc gagcgcccaa   60
acctgaactt aagctatttg gggctacttg tatttggaaa aaatatatcg ggtcctttac   120
tggtccgccg gtgttatttt aacttatgaa atg gtt ggt ttt tgc agt gca tta   174
                                   Met Val Gly Phe Cys Ser Ala Leu
                                    1   5

gat tta cag caa cgg att ggt ttg gcc aac acg ttg agt tca ggt tca   222
Asp Leu Gln Gln Arg Ile Gly Leu Ala Asn Thr Leu Ser Ser Gly Ser
        10   15   20

atg tct gaa cca gca caa cct agt gga ggg gaa ggt gat gtc aac acg   270
Met Ser Glu Pro Ala Gln Pro Ser Gly Gly Glu Gly Asp Val Asn Thr
25   30   35   40

ctc cga ata ctt gta gca acc gac tgc cat cta ggc tac atg gag aaa   318
Leu Arg Ile Leu Val Ala Thr Asp Cys His Leu Gly Tyr Met Glu Lys
                 45   50   55

gat gag ata cgt agg ttt gat tcc ttt caa gca ttt gag gag att tgc   366
Asp Glu Ile Arg Arg Phe Asp Ser Phe Gln Ala Phe Glu Glu Ile Cys
             60   65   70

gca ttg gca gat aaa aat aag gtg gat ttt ata ctt ctc ggt ggt gat   414
Ala Leu Ala Asp Lys Asn Lys Val Asp Phe Ile Leu Leu Gly Gly Asp
         75   80   85

1

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cta ttc cat gag aac aag ccg tca cgc tca acc ctg gta aaa acg att      462
Leu Phe His Glu Asn Lys Pro Ser Arg Ser Thr Leu Val Lys Thr Ile
    90                    95                  100

gag att cta cgg cgc tac tgc cta aat gat caa cct gtg aag ttc cag      510
Glu Ile Leu Arg Arg Tyr Cys Leu Asn Asp Gln Pro Val Lys Phe Gln
105                   110               115                   120

gtt gtc agt gat cag aca gtt aac ttt cca aac agg ttt ggt aag gta      558
Val Val Ser Asp Gln Thr Val Asn Phe Pro Asn Arg Phe Gly Lys Val
                  125               130                   135

aat tat gaa gac cca aac ttt aac gtt ggt ctg cct gtg ttc acc att      606
Asn Tyr Glu Asp Pro Asn Phe Asn Val Gly Leu Pro Val Phe Thr Ile
              140                   145               150

cat gga aat cat gat gac cct gct gga gtg gat aat ctc tct gct atc      654
His Gly Asn His Asp Asp Pro Ala Gly Val Asp Asn Leu Ser Ala Ile
              155                   160               165

gat att ctt tcg gct tgc aat ctt gta aat tat ttt gga aag atg gac      702
Asp Ile Leu Ser Ala Cys Asn Leu Val Asn Tyr Phe Gly Lys Met Asp
    170                   175               180

ctt ggt ggc tct ggc gtt ggt cag ata gca gtt tat cct gta ctt gta      750
Leu Gly Gly Ser Gly Val Gly Gln Ile Ala Val Tyr Pro Val Leu Val
185                   190               195                   200

aaa aag ggc atg act tca gtt gca ctg tat ggt ctt gga aac att aga      798
Lys Lys Gly Met Thr Ser Val Ala Leu Tyr Gly Leu Gly Asn Ile Arg
                  205               210                   215

gat gaa cga cta aat aga atg ttt cag acg cct cat tca gta cag tgg      846
Asp Glu Arg Leu Asn Arg Met Phe Gln Thr Pro His Ser Val Gln Trp
              220                   225               230

atg cga cct gga act caa gat ggg gag tca gcg tct gac tgg ttc aat      894
Met Arg Pro Gly Thr Gln Asp Gly Glu Ser Ala Ser Asp Trp Phe Asn
              235               240                   245

ata ttg gta ctt cat cag aat agg ata aag aca aac cct aaa agt gcc      942
Ile Leu Val Leu His Gln Asn Arg Ile Lys Thr Asn Pro Lys Ser Ala
    250                   255               260

atc aat gag cat ttc tta cca ggt tca tca gtc gcg acg tcc ctg att      990
Ile Asn Glu His Phe Leu Pro Gly Ser Ser Val Ala Thr Ser Leu Ile
265                   270               275                   280

gat ggt gaa gca aaa cca aag cat gtt ctt ttg tta gaa atc aag gga     1038
Asp Gly Glu Ala Lys Pro Lys His Val Leu Leu Leu Glu Ile Lys Gly
                  285               290                   295

aat cag tac agg cca acc aaa ata cct ctg aga tct gtc aga cct ttt     1086
Asn Gln Tyr Arg Pro Thr Lys Ile Pro Leu Arg Ser Val Arg Pro Phe
                  300               305                   310
```

2

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gaa tat gct gag gtt gtg ttg aaa gat gaa gca gat gtt aac tca aat    1134
Glu Tyr Ala Glu Val Val Leu Lys Asp Glu Ala Asp Val Asn Ser Asn
        315                 320                 325


gat cag gac tct gtg ctt gaa cat ttg gat aaa att gta aga aat ctg    1182
Asp Gln Asp Ser Val Leu Glu His Leu Asp Lys Ile Val Arg Asn Leu
        330                 335                 340


att gag aag agt agc caa cca act gcc agc aga tca gag ccc aaa ctt    1230
Ile Glu Lys Ser Ser Gln Pro Thr Ala Ser Arg Ser Glu Pro Lys Leu
345                 350                 355                 360


cca tta gtt aga atc aag gta gat tac tct ggg ttt tca aca ata aac    1278
Pro Leu Val Arg Ile Lys Val Asp Tyr Ser Gly Phe Ser Thr Ile Asn
                365                 370                 375



cca caa cgt ttt ggt cag aag tat gtt gga aag gtc gca aac cct caa    1326
Pro Gln Arg Phe Gly Gln Lys Tyr Val Gly Lys Val Ala Asn Pro Gln
                380                 385                 390


gat att ctc att ttc tca aaa tca gca aag aag cgc cag act aca gga    1374
Asp Ile Leu Ile Phe Ser Lys Ser Ala Lys Lys Arg Gln Thr Thr Gly
        395                 400                 405


gat cac att gat gat tct gag aaa ctt cgt cct gag gaa cta aac caa    1422
Asp His Ile Asp Asp Ser Glu Lys Leu Arg Pro Glu Glu Leu Asn Gln
        410                 415                 420


caa aca atc gaa gct ctg gtc gca gag agt aac ttg aaa atg gag att    1470
Gln Thr Ile Glu Ala Leu Val Ala Glu Ser Asn Leu Lys Met Glu Ile
425                 430                 435                 440


ctt ccg gtt gat gat ttg gac att gcg ttg cat gat ttt gtg aac aag    1518
Leu Pro Val Asp Asp Leu Asp Ile Ala Leu His Asp Phe Val Asn Lys
                445                 450                 455


gat gac aag atg gca ttt tat tca tgt ttg cag aga aac ctt gaa gaa    1566
Asp Asp Lys Met Ala Phe Tyr Ser Cys Leu Gln Arg Asn Leu Glu Glu
                460                 465                 470


acc agg aat aag ttg agt tct gaa gca gat aaa tcc aaa ttt gag gaa    1614
Thr Arg Asn Lys Leu Ser Ser Glu Ala Asp Lys Ser Lys Phe Glu Glu
        475                 480                 485


gaa gat ata ata gtc aaa gtt ggc gag tgc atg cag gag cgc gtt aag    1662
Glu Asp Ile Ile Val Lys Val Gly Glu Cys Met Gln Glu Arg Val Lys
        490                 495                 500


gaa agg tct ctg cac tct aag gac ggc aca cgt ttg aca aca ggc tct    1710
Glu Arg Ser Leu His Ser Lys Asp Gly Thr Arg Leu Thr Thr Gly Ser
505                 510                 515                 520


cac aac ttg gtg ttt aat tat ctg agc ctt aat atc ttt tct ttt tgt    1758
His Asn Leu Val Phe Asn Tyr Leu Ser Leu Asn Ile Phe Ser Phe Cys
```

3

```
att ttt cct ggg gct gga tac tgg aca gct agt aac tct tac aac ctt      1806
Ile Phe Pro Gly Ala Gly Tyr Trp Thr Ala Ser Asn Ser Tyr Asn Leu
            540                 545                 550
```

```
taactaggat actggaggta aatcttttac agctcaaagc aaccagaact ccttcagtga     1866
tgatgaagac accaggggaga tgcttcttgg tgcaagatca actgatgttg gacgaaaatc    1926
atctggattt actagaccct ccaaagatac tgctgatgtt gctaaacgtg gtacttccaa     1986
aagaggcagg ggaagaggca ccagttcaat gaagcagacc actcttagtt tcagccagtc     2046
aaggtcagct accgttattc gtagtgagga tgtggcttcc tctgaggagg aagcagatgc     2106
aaatgaagtt gttgaaaatt cagaagagga gagtgcgcaa caagttggac gtaaaagagc     2166
agctcctagg ggtagaggta gaggtagagg cggaggttcc actgcaaaga ggggggcgaaa    2226
aacagatatt gcttccatgc aaaatatgat gagcaaagat gatgatgatt cagaagatga     2286
accgccaaag aaaactcctc gggtcaccag gaactatggc gctgtcagga ggagatgacc     2346
ctttaaggag ttcttgctca tgagagttat aggctaggtg ttttgtcttg taaagttgga     2406
agagccgacg tgttttatc aaccttgacg tcgaccagtt tgcgttgccg tgaactgact     2466
gtaccttgta cacgcccgaa tgtaacggat ttttgggatt tatacatcct tgtagctgct    2526
taaattccag cgattgctgt caaatgaact tcgggaaaaa aaaaaaaaaa aaaaaaaaaa     2586
aaaaaaaaaa a                                                          2597
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    <210> 2
    <211> 552
    <212> PRT
    <213> Zea mays

    <400> 2
Met Val Gly Phe Cys Ser Ala Leu Asp Leu Gln Gln Arg Ile Gly Leu
1               5                   10                  15
Ala Asn Thr Leu Ser Ser Gly Ser Met Ser Glu Pro Ala Gln Pro Ser
        20                  25                  30
Gly Gly Glu Gly Asp Val Asn Thr Leu Arg Ile Leu Val Ala Thr Asp
        35                  40                  45
Cys His Leu Gly Tyr Met Glu Lys Asp Glu Ile Arg Arg Phe Asp Ser
    50                  55                  60
Phe Gln Ala Phe Glu Glu Ile Cys Ala Leu Ala Asp Lys Asn Lys Val
65                  70                  75                  80
Asp Phe Ile Leu Leu Gly Gly Asp Leu Phe His Glu Asn Lys Pro Ser
                85                  90                  95
Arg Ser Thr Leu Val Lys Thr Ile Glu Ile Leu Arg Arg Tyr Cys Leu
            100                 105                 110
Asn Asp Gln Pro Val Lys Phe Gln Ile Val Val Ser Asp Gln Thr Val Asn
        115                 120                 125
Phe Pro Asn Arg Phe Gly Lys Val Asn Tyr Glu Asp Pro Asn Phe Asn
    130                 135                 140
Val Gly Leu Pro Val Phe Thr Ile His Gly Asn His Asp Asp Pro Ala
145                 150                 155                 160
Gly Val Asp Asn Leu Ser Ala Ile Asp Ile Leu Ser Ala Cys Asn Leu
                165                 170                 175
Val Asn Tyr Phe Gly Lys Met Asp Leu Gly Gly Ser Gly Val Gly Gln
            180                 185                 190
Ile Ala Val Tyr Pro Val Leu Val Lys Lys Gly Met Thr Ser Val Ala
        195                 200                 205
Leu Tyr Gly Leu Gly Asn Ile Arg Asp Glu Arg Leu Asn Arg Met Phe
    210                 215                 220
Gln Thr Pro His Ser Val Gln Trp Met Arg Pro Gly Thr Gln Asp Gly
```

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225                    230                  235                    240
Glu Ser Ala Ser Asp Trp Phe Asn Ile Leu Val Leu His Gln Asn Arg
            245                  250                  255
Ile Lys Thr Asn Pro Lys Ser Ala Ile Asn Glu His Phe Leu Pro Gly
            260                  265                  270
Ser Ser Val Ala Thr Ser Leu Ile Asp Gly Glu Ala Lys Pro Lys His
        275                  280                  285
Val Leu Leu Leu Glu Ile Lys Gly Asn Gln Tyr Arg Pro Thr Lys Ile
    290                  295                  300
Pro Leu Arg Ser Val Arg Pro Phe Glu Tyr Ala Glu Val Val Leu Lys
305                  310                  315                  320
Asp Glu Ala Asp Val Asn Ser Asn Asp Gln Asp Ser Val Leu Glu His
            325                  330                  335
Leu Asp Lys Ile Val Arg Asn Leu Ile Glu Lys Ser Ser Gln Pro Thr
        340                  345                  350
Ala Ser Arg Ser Glu Pro Lys Leu Pro Leu Val Arg Ile Lys Val Asp
        355                  360                  365
Tyr Ser Gly Phe Ser Thr Ile Asn Pro Gln Arg Phe Gly Gln Lys Tyr
    370                  375                  380
Val Gly Lys Val Ala Asn Pro Gln Asp Ile Leu Ile Phe Ser Lys Ser
385                  390                  395                  400
Ala Lys Lys Arg Gln Thr Thr Gly Asp His Ile Asp Asp Ser Glu Lys
            405                  410                  415
Leu Arg Pro Glu Glu Leu Asn Gln Thr Ile Glu Ala Leu Val Ala
        420                  425                  430
Glu Ser Asn Leu Lys Met Glu Ile Leu Pro Val Asp Asp Leu Asp Ile
        435                  440                  445
Ala Leu His Asp Phe Val Asn Lys Asp Asp Lys Met Ala Phe Tyr Ser
    450                  455                  460
Cys Leu Gln Arg Asn Leu Glu Glu Thr Arg Asn Lys Leu Ser Ser Glu
465                  470                  475                  480
Ala Asp Lys Ser Lys Phe Glu Glu Glu Asp Ile Ile Val Lys Val Gly
        485                  490                  495
Glu Cys Met Gln Glu Arg Val Lys Glu Arg Ser Leu His Ser Lys Asp
        500                  505                  510
Gly Thr Arg Leu Thr Thr Gly Ser His Asn Leu Val Phe Asn Tyr Leu
        515                  520                  525
Ser Leu Asn Ile Phe Ser Phe Cys Ile Phe Pro Gly Ala Gly Tyr Trp
    530                  535                  540
Thr Ala Ser Asn Ser Tyr Asn Leu
545                  550

        <210> 3
        <211> 36
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Designed oligonucleotide based upon an adaptor
              used for cDNA library construction and poly(dT) to
              remove clones which have a poly(A) tail but no
              cDNA insert.


        <400> 3
tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa                                    36
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5

<210> 4
<211> 2308
<212> DNA
<213> Zea mays

<400> 4
ccgactgcca tctaggctac atggagaaag atgagatacg taggtttgat tcctttcaag   60
catttgagga gatttgcgca ttggcagata aaaataaggt ggatttata cttctcggtg   120
gtgatctatt ccatgagaac aagccgtcac gctcaaccct ggtaaaaacg attgagattc   180
tacgcgcta ctgcctaaat gatcaacctg tgaagttcca ggttgtcagt gatcagacag   240
ttaactttcc aaacaggttt ggtaaggtaa attatgaaga cccaaacttt aacgttggtc   300
tgcctgtgtt caccattcat ggaaatcatg atgacctgc tggagtggat aatctctctg   360
ctatcgatat tctttcggct tgcaatcttg taaattattt tggaaagatg gaccttggtg   420
gctctggcgt tggtcagata gcagtttatc ctgtacttgt aaaaaagggc atgacttcag   480
ttgcactgta tggtcttgga aacattagag atgaacgact aaatagaatg tttcagacgc   540
ctcattcagt acagtggatg cgacctggaa ctcaagatgg ggagtcagcg tctgactggt   600
tcaatatatt ggtacttcat cagaataggga taaagacaaa ccctaaaagt gccatcaatg   660
agcatttctt accaggttca tcagtcgcga cgtccctgat tgatggtgaa gcaaaaccaa   720
agcatgttct tttgttagaa atcaagggaa atcagtacag gccaaccaaa atacctctga   780
gatctgtcag acctttgaa tatgctgagg ttgtgttgaa agatgaagca gatgttaact   840
caaatgatca ggactctgtg cttgaacatt tggataaaat tgtaagaaat ctgattgaga   900
agagtagcca accaactgcc agcagatcga agcccaaact tccattagtt agaatcaagg   960
tagattactc tgggttttca acaataaacc cacaacgttt tggtcagaag tatgttggaa   1020
aggtcgcaaa ccctcaagat attctcattt tctcaaaatc agcaaagaag cgccagacta   1080
caggagatca cattgatgat tctgagaaac ttcgtcctga ggaactaaac caacaaacaa   1140
tcgaagctct ggtcgcagag agtaacttga aaatggagat tcttccggtt gatgatttgc   1200
acattgcgtt gcatgatttt gtgaacaagg atgacaagat ggcattttat tcatgtttgc   1260
agagaaacct tgaagaaacc aggaataagt tgagttctga acagataaa tccaaatttg   1320
aggaagaaga tataatagtc aaagttggcg agtgcatgca ggaacgcgtt aaggaaaggt   1380
ctctgcactc taaggacggc acacgtttga caacaggctc tcacaacttg gtgtttaatt   1440
atctgagcct taatatcttt tcttttgta ttttcctgg ggctggatac tggacagcta   1500
gtaactctta caaccttaa ctaggatact ggaggtaaat cttttacagc tcaaagcaac   1560
cagaactcct tcagtgatga tgaagacacc agggagatgc ttcttggtgc aagatcaact   1620
gatgttggac gaaaatcatc tggatttact agaccctcca aagatactgc tgatgttgct   1680
aaacgtggta cttccaaaag aggcaggggga agaggcacca gttcaatgaa gacgaccact   1740
cttagtttca gccagtcaag gtcagctacc gttattcgta gtgaggatgt ggcttcctct   1800
gaggaggaag cagatgcaaa tgaagttgtt gaaaattcag aagaggagag tgcgcaacaa   1860
gttgacgta aaagagcagc tcctaggggt agaggtagag gtagaggcgg aggttccact   1920
gcaaagaggg ggcgaaaaac agatattgct tccatgcaaa atgatgatgg caaagatgat   1980
gatgattcag aagatgaacc gccaaagaaa actcctcggg tcaccaggaa ctatggcgct   2040
gtcaggagga gatgacccct taaggagttc ttgctcatga gagttatagg ctaggtgtt   2100
tgtcttgtaa agttggaaga gccgacgtgt tttatcaac cttgacgtcg accagtttgc   2160
gttgccgtga actgactgta ccttgtacac gcccgaatgt aaccgatttt tgggatttat   2220
acatcctgt agctgcttaa attccagcga ttgctgtcaa atgaacttcg ggaaaaaaa   2280
aaaaaaaaaa aaaaaaaaaa aaaaaaaa   2308

<210> 5
<211> 396
<212> DNA
<213> Zea mays

<400> 5
tcgacccacg cgtccggccg gcccttctct tcccttgctg ctgtgcgaac ccgagcgccc   60
aaacctgaac ttaagctatt tggggctact tgtatttgga aaaaatatat cgggtccttt   120
actggtccgc cggtgttatt ttaacttatg aaatggttgg tttttgcagt gcattagatt   180

6

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tacagcaacg gattggtttg gccaacacgt tgagttcagg ttcaatgtct gaaccagcac      240
aacctagtgg aggggaaggt gatgtcaaca cgctcctaat acttgtagca accgactgcc      300
atctaggcta catggagaaa gatgagatac gtaggtttga ttcctttcaa gcatttgagg      360
agatttgcgc attggcagat aaaaataagg tggatt                                396

        <210> 6
        <211> 36
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> M13R synthetic primer

        <400> 6
agcggataac aatttcacac aggaaacagc tatgac                                 36

        <210> 7
        <211> 20
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> R1 synthetic primer

        <400> 7
cttattttta tctgccaatg                                                   20

        <210> 8
        <211> 25
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> T7 synthetic primer

        <400> 8
taatacgact cactataggg cgaat                                             25

        <210> 9
        <211> 20
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> R2 synthetic primer

        <400> 9
gcgtgacggc ttgttctcat                                                   20
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